SEQUENCE LISTING

<110> Commonwealth Scientific and Industrial Reseach Organization

<120> Efficient gene silencing in plants using short dsRNA sequences

<130> BCS-03-2001

<150> US 60/447,711

<151> 2003-02-19

<160> 33

<170> PatentIn version 3.1

<210> 1

<211> 341

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the promoter of the 7SL-2 gene of Arabidopsis thalian
       a var. Landsberg erecta

<220>

<221> misc_feature

<222> (1)..(6)

<223> XhoI restriction site

<220>

<221> misc_feature

<222> (7)..(322)

<223> PolIII promoter region

<220>

<221> misc_feature

<222> (336)..(341)

<223> XhoI restriction site

<220>

<221> misc_feature

<222> (329)..(335)

<223> poly T nucleotide stretch

<220>

<221> misc_feature

<222> (323)..(328)

<223> SalI restriction site


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ctcgagatgt tgttgttacc agaaagtaaa taaatgttca atctctgatg ttctcaagta      60
agtgagtttt attgggaata atattaactc atgttcttct gcatttgatt cctttgccgc     120
tctcttcttc tatcttaaat ctgtgtatac tatttcacta ttgggctttt tattagtcta     180
taatgggact caaaataagg ctttggccca catcaaaaag ataagtcaca aatcaaaact     240
aaattcagag tcttttctcc cacatcggtc actgtactca ttttgtgttt gtttatatat     300
tacacgaacc gatctttgtt acgtcgactt tttttctcga g                        341
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<210> 2

<211> 429

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the promoter of the 7SL-2 gene of Arabidopsis thalian
       a var. Landsberg erecta including 86 bases downstream of the tran
       scription initiation site.

<220>

<220>

<221> misc_feature

<222> (1)..(6)

<223> XhoI restriction site

<220>

<221> misc_feature

<222> (424)..(429)

<223> XhoI restriction site

<220>

<221> misc_feature

<222> (415)..(423)

<223> poly T stretch

<220>

<221> misc_feature

<222> (409)..(414)

<223> SalI restriction site

<220>

<221> misc_feature

<222> (7)..(408)

<223> PolIII promoter region.

<400> 2
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ctcgagatgt tgttgttacc agaaagtaaa taaatgttca atctctgatg ttctcaagta      60
agtgagtttt attgggaata atattaactt atgttcttct tgcatttgat ttctttgccg     120
ctctcttctt ctatcttaaa tctgtgtata ctatttcact attgggcttt ttattagtct     180
ataatgggac tcaaaataag gctttggccc acatcaaaaa gataagtcac aaatcaaaac     240
taaattcaga gtcttttctc ccacatcggt cactgtactc ttttgtgttt gtttatatat     300
tacacgaacc gatctttggt acgtcgagct aagtaacatg agcttgtaac ccatgtgggg     360
acattaagat ggtggaacac tggctcgggt ccacgggccg gttctgttgt cgactttttt     420
tttctcgag                                                            429
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<210> 3

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<211>  334

<212>  DNA

<213>  Artificial Sequence


<220>

<223>  sequence of the promoter of the U3 snRNA of Arabidopsis thaliana
       var. Landsberg erecta

<220>

<221>  misc_feature

<222>  (1)..(6)

<223>  EcoRI restriction site


<220>

<221>  misc_feature

<222>  (314)..(319)

<223>  PvuI restriction site


<220>

<221>  misc_feature

<222>  (320)..(328)

<223>  poly T stretch


<220>

<221>  misc_feature

<222>  (329)..(334)

<223>  EcoRI restriction site


<220>

<221>  misc_feature

<222>  (7)..(313)

<223>  Pol III promoter region
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<400>  3
gaattcttat gcagcctgtg atggataact gaatcaaaca aatggcgtct gggtttaaga     60
agatctgttt tggctatgtt ggacgaaaca agtgaacttt taggatcaac ttcagtttat    120
atatggagct tatatcgagc aataagataa gtgggctttt tatgtaattt aatgggctat    180
cgtccataga ttcactaata cccatgccca gtacccatgt atgcgtttca tataagctcc    240
taatttctcc cacatcgctc aaatctaaac aaatcttgtt gtatatataa cactgaggga    300
gcaacattgg tcacgatcgt ttttttttga attc                                 334
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<210> 4

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the promoter of the U3 snRNA gene of Arabidopsis thal
        iana var. Landsberg erecta including 136 bases downstream of the
        transcription initiation site.

<220>

<221> misc_feature

<222> (1)..(6)

<223> EcoRI restriction site

<220>

<221> misc_feature

<222> (7)..(446)

<223> Pol III promoter region

<220>

<221> misc_feature

<222> (447)..(452)

<223> XhoI restriction site

<220>

<221> misc_feature

```
<222>   (453)..(461)

<223>   poly T stretch



<220>

<221>   misc_feature

<222>   (462)..(467)

<223>   EcoRI restriction site



<400>   4
gaattcttat gcagcctgtg atggataact gaatcaaaca aatggcgtct gggtttaaga      60
agatctgttt tggctatgtt ggacgaaaca agtgaacttt taggatcaac ttcagtttat     120
atatggagct tatatcgagc aataagataa gtgggctttt tatgtaattt aatgggctat     180
cgtccataga ttcactaata cccatgccca gtacccatgt atgcgtttca tataagctcc     240
taatttctcc cacatcgctc aaatctaaac aaatcttgtt gtatatataa cactgaggga     300
gcaacattgg tcacgacctt acttgaacag gatctgttct ataggctcgt acctctgttt     360
ccttgatttc tcaagagaca ggcccttaac cctggttgat gaaccatgac cgtgcggcta     420
gagcgtgatt gacggctacg atcgtcctcg agtttttttt tgaattc                   467



<210>   5

<211>   456

<212>   DNA

<213>   Artificial Sequence



<220>

<223>   sequence of the promoter of the U6 snRNA gene of Arabidopsis thal
        iana var. Landsberg erecta including 3 bases downstream of the tr
        anscription initiation site

<220>

<221>   misc_feature

<222>   (1)..(6)

<223>   XhoI restriction site



<220>

<221>   misc_feature

<222>   (7)..(436)

<223>   Pol III promoter region
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<220>

<221> misc_feature

<222> (437)..(442)

<223> SalI restriction site

<220>

<221> misc_feature

<222> (443)..(450)

<223> poly T stretch

<220>

<221> misc_feature

<222> (451)..(456)

<223> Sac I restriction site


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<400> 5
ctcgagcttc gttgaacaac ggaaactcga cttgccttcc gcacaataca tcatttcttc      60
ttagcttttt ttcttcttct tcgttcatac agtttttttt tgtttatcag cttacatttt     120
cttgaaccgt agctttcgtt ttcttctttt taactttcca ttcggagttt ttgtatcttg     180
tttcatagtt tgtcccagga ttagaatgat taggcatcga accttcaaga atttgattga     240
ataaaacatc ttcattctta agatatgaag ataatcttca aaaggccct gggaatctga      300
aagaagagaa gcaggcccat ttatatggga aagaacaata gtatttctta tataggccca     360
tttaagttga aaacaatctt caaaagtccc acatcgctta gataagaaaa cgaagctgag     420
tttatataca gctagagtcg actttttttt gagctc                              456
```

<210> 6

<211> 488

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the promoter of the U3 snRNA gene of Arabidopsis thal
      iana var. Landsberg erecta including 20 bases downstream of the t
      ranscription initiation site

<220>

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<221>  misc_feature

<222>  (1)..(6)

<223>  XhoI restriction site


<220>

<221>  misc_feature

<222>  (7)..(468)

<223>  Pol III promoter region


<220>

<221>  misc_feature

<222>  (469)..(474)

<223>  PvuI restriction site


<220>

<221>  misc_feature

<222>  (475)..(482)

<223>  Poly T stretch


<220>

<221>  misc_feature

<222>  (483)..(488)

<223>  XhoI restriction site


<400>  6
ctcgagcttc gttgaacaac ggaaactcga cttgccttcc gcacaataca tcatttcttc      60
ttagcttttt ttcttcttct tcgttcatac agtttttttt tgtttatcag cttacatttt     120
cttgaaccgt agctttcgtt ttcttctttt taactttcca ttcggagttt ttgtatcttg     180
tttcatagtt tgtcccagga ttagaatgat taggcatcga accttcaaga atttgattga     240
ataaaacatc ttcattctta agatatgaag ataatcttca aaaggcccct gggaatctga     300
aagaagagaa gcaggcccat ttatatggga aagaacaata gtatttctta tataggccca     360
tttaagttga aaacaatctt caaaagtccc acatcgctta gataagaaaa cgaagctgag     420
tttatataca gctagagtcg aagtagtgat tgtcccttcg gggacatccg atcgtttttt     480
ttctcgag                                                             488
```

```
<210>  7

<211>  405

<212>  DNA

<213>  Artificial Sequence


<220>

<223>  sequence of the promoter of the U3 snRNA of rice (Oryza sativa In
       dica IR36)

<220>

<221>  misc_feature

<222>  (1)..(6)

<223>  EcoRI restriction site


<220>

<221>  misc_feature

<222>  (7)..(384)

<223>  Pol III promoter region


<220>

<221>  misc_feature

<222>  (385)..(390)

<223>  PvuI restriction site


<220>

<221>  misc_feature

<222>  (391)..(399)

<223>  poly T stretch


<220>

<221>  misc_feature

<222>  (400)..(405)
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<223> EcoRI restriction site

<400> 7
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gaattcaagg gatctttaaa catacgaaca gatcacttaa agttcttctg aagcaactta    60
aagttatcag gcatgcatgg atcttggagg aatcagatgt gcagtcaggg accatagcac   120
aggacaggcg tcttctactg gtgctaccag caaatgctgg aagccgggaa cactgggtac   180
gttggaaacc acgtgatgtg gagtaagata aactgtagga gaaaagcatt tcgtagtggg   240
ccatgaagcc tttcaggaca tgtattgcag tatgggccgg cccattacgc aattggacga   300
caacaaagac tagtattagt accacctcgg ctatccacat agatcaaagc tggtttaaaa   360
gagttgtgca gatgatccgt ggcacgatcg tttttttttg aattc                   405
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<210> 8

<211> 442

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the promoter of the U3 snRNA of tomato (a garden vari
      ety with small gourd-shaped yellow fruit)

<220>

<221> misc_feature

<222> (1)..(6)

<223> EcoRI restriction site

<220>

<221> misc_feature

<222> (7)..(421)

<223> Pol III promoter region

<220>

<221> misc_feature

<222> (422)..(427)

<223> PvuI restriction site

<220>

<221> misc_feature

<222> (428)..(436)

<223> Poly T stretch

<220>

<221> misc_feature

<222> (437)..(442)

<223> EcoRI restriction site

<400> 8
gaattctgag agcattgtgt ggcgttcctc tgaattactt actgtcactt tgattggagc   60
cattattttc agactctact gaagattgaa ttgaatgaga aactatgaaa ctttacaagt   120
gaattattat ggagttcatg gcaactgcta tggagttttt cctactggga attggaacgg   180
tttctacgaa attaactgtc cacacgttaa aaatataaat taatgcgtaa ttgttatttt   240
ttctataaca aataaaaaac tgaaatacga cataaatttt attactttaa ttgcacttta   300
gccttagaga tattgcgttg tagtcggcgt aggtgtgtca ggggccaata tattgttccc   360
acatcggcag tgcagcacat aaactctagc gttataagaa tctatccact atcaacggtc   420
acgatcgttt tttttgaat tc   442

<210> 9

<211> 295

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the dsRNA encoding region of 94bp for silencing expre
     ssion of the GUS gene (GUShp94)

<220>

<221> misc_feature

<222> (1)..(6)

<223> SalI restriction site

<220>

<221> misc_feature

<222> (6)..(11)

<223> PvuI restriction site

<220>

<221> misc_feature

<222> (12)..(100)

<223> GUS sequence (sense)

<220>

<221> misc_feature

<222> (101)..(195)

<223> spacer sequence

<220>

<221> misc_feature

<222> (190)..(195)

<223> BamHI restriction site

<220>

<221> misc_feature

<222> (196)..(284)

<223> GUS sequence (antisense)

<220>

<221> misc_feature

<222> (285)..(290)

<223> PvuI restriction site

<220>

<221> misc_feature

<222> (290)..(295)

<223> SalI restriction site

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<400>  9
gtcgacgatc gcagcgtaat gctctacacc acgccgaaca cctgggtgga cgatatcacc      60
gtggtgacgc atgtcgcgca agactgtaac cacgcgtctg ttgactggca ggtggtggcc     120
aatggtgatg tcagcgttga actgcgtgat gcggatcaac aggtggttgc aactggacaa     180
ggcactagcg ggatccagac gcgtggttac agtcttgcgc gacatgcgtc accacggtga     240
tatcgtccac ccaggtgttc ggcgtggtgt agagcattac gctgcgatcg tcgac         295
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<210>  10

<211>  93

<212>  DNA

<213>  Artificial Sequence


<220>

<223>  sequence of the dsRNA encoding region of 41 bp for silencing expr
       ession of the GUS gene (GUShp41)

<220>

<221>  misc_feature

<222>  (1)..(6)

<223>  SalI restriction site


<220>

<221>  misc_feature

<222>  (7)..(42)

<223>  GUS sequence (sense)


<220>

<221>  misc_feature

<222>  (43)..(51)

<223>  spacer sequence


<220>

<221>  misc_feature

<222>  (52)..(87)
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<223> GUS sequence (antisense)

<220>

<221> misc_feature

<222> (88)..(93)

<223> Sal I restriction site

<400> 10
gtcgactggg cagatgaaca tggcatcgtg gtgattgatg aatgcgagaa cttcatcaat   60
caccacgatg ccatgttcat ctgcccagtc gac   93

<210> 11

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the dsRNA encoding region of 21 bp for silencing expr
      ession of the GUS gene (GUShp21)

<220>

<221> misc_feature

<222> (1)..(6)

<223> SalI restriction site

<220>

<221> misc_feature

<222> (7)..(22)

<223> GUS sequence (sense)

<220>

<221> misc_feature

<222> (23)..(28)

<223> spacer sequence

<220>

<221> misc_feature

<222> (29)..(44)

<223> GUS sequence (antisense)

<220>

<221> misc_feature

<222> (45)..(50)

<223> Sal I restriction site

<400> 11
gtcgactggg cagatgaaca tgtacgatca tgttcatctg cccagtcgac   50

<210> 12

<211> 94

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the dsRNA encoding region of 42 bp for silencing expr
      ession of the PHYB gene, derived from the 5' end of PHYB (PHYB5hp
      42)-upper strand

<400> 12
tcgacggagt cgggggtagt ggcggtggcc gtggcggtgg ccgtggagga ggccacggcc   60
accgccacgg ccaccgccac tacccccgac tccg   94

<210> 13

<211> 94

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the dsRNA encoding region of 42 bp for silencing expr

ession of the PHYB gene, derived from the 5' end of PHYB (PHYB5hp 42)-lower strand

<400> 13
tcgacggagt cggggtagt ggcggtggcc gtggcggtgg ccgtggcctc ctccacggcc   60
accgccacgg ccaccgccac tacccccgac tccg   94

<210> 14

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the dsRNA encoding region of 21 bp for silencing expr ession of the PHYB gene, derived from the 5' end of PHYB (PHYB5hp 21)-upper strand

<400> 14
tcgacggagt cggggtagt ggcggaggag ccgccacta cccccgactc cg   52

<210> 15

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the dsRNA encoding region of 21 bp for silencing expr ession of the PHYB gene, derived from the 5' end of PHYB (PHYB5hp 21)-lower strand

<400> 15
tcgacggagt cggggtagt ggcggcctcc tccgccacta cccccgactc cg   52

<210> 16

<211> 94

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the dsRNA encoding region of 42 bp for silencing expr

ession of the PHYB gene, derived from the center of PHYB (PHYBChp
42)-upper strand

<400> 16
tcgatggatg gtgtggttca gccatgtagg gatatggcgg gggaacagga gggttccccc   60
gccatatccc tacatggctg aaccacacca tcca   94

<210> 17

<211> 94

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the dsRNA encoding region of 42 bp for silencing expr
ession of the PHYB gene, derived from the center of PHYB (PHYBChp
42)-lower strand

<400> 17
tcgatggatg gtgtggttca gccatgtagg gatatggcgg gggaaccctc ctgttccccc   60
gccatatccc tacatggctg aaccacacca tcca   94

<210> 18

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the dsRNA encoding region of 21 bp for silencing expr
ession of the PHYB gene, derived from the center of PHYB (PHYBChp
21)-upper strand

<400> 18
tcgatggatg gtgtggttca gccataggag gatggctgaa ccacacctcc aa   52

<210> 19

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223>   sequence of the dsRNA encoding region of 21 bp for silencing expr
          ession of the PHYB gene, derived from the center of PHYB (PHYBChp
          21)-lower strand

<400> 19
tcgatggatg gtgtggttca gccatcctcc tatggctgaa ccacaccatc ca   52

<210> 20

<211> 94

<212> DNA

<213> Artificial Sequence

<220>

<223>   sequence of the dsRNA encoding region of 42 bp for silencing expr
          ession of the PHYB gene, derived from the 3' end of PHYB (PHYB3hp
          42)-upper strand

<400> 20
tcgacattgt caactgctag tggaagtggt gacatgatgc tgatgaagga ggtcatcagc   60
atcatgtcac cacttccact agcagttgac aatg   94

<210> 21

<211> 94

<212> DNA

<213> Artificial Sequence

<220>

<223>   sequence of the dsRNA encoding region of 42 bp for silencing expr
          ession of the PHYB gene, derived from the 3' end of PHYB (PHYB3hp
          42)-lower strand

<400> 21
tcgacattgt caactgctag tggaagtggt gacatgatgc tgatgacctc cttcatcagc   60
atcatgtcac cacttccact agcagttgac aatg   94

<210> 22

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223>   sequence of the dsRNA encoding region of 21 bp for silencing expr
         ession of the PHYB gene, derived from the 3' end of PHYB (PHYB3hp
         21)-upper strand

<400>   22
tcgacattgt caactgctag tggaaaggag gttccactag cagttgacaa tg   52

<210>   23

<211>   52

<212>   DNA

<213>   Artificial Sequence

<220>

<223>   sequence of the dsRNA encoding region of 21 bp for silencing expr
         ession of the PHYB gene, derived from the 3' end of PHYB (PHYB3hp
         21)-lower strand

<400>   23
tcgacattgt caactgctag tggaacctcc tttccactag cagttgacaa tg   52

<210>   24

<211>   94

<212>   DNA

<213>   Artificial Sequence

<220>

<223>   sequence of the dsRNA encoding region of 42 bp for silencing expr
         ession of the PDS gene (PDS42)-upper strand

<400>   24
tcgacttaac ttgtaaggaa tattacgatc ctaaccggtc aatgctagga ggagcattga   60
ccggttagga tcgtaatatt ccttacaagt taag   94

<210>   25

<211>   94

<212>   DNA

<213>   Artificial Sequence

<220>

<223>   sequence of the dsRNA encoding region of 42 bp for silencing expr
         ession of the PDS gene (PDS42)-lower strand

<400>   25
tcgacttaac ttgtaaggaa tattacgatc ctaaccggtc aatgctcctc ctagcattga   60
ccggttagga tcgtaatatt ccttacaagt taag   94

<210>   26

<211>   52

<212>   DNA

<213>   Artificial Sequence

<220>

<223>   sequence of the dsRNA encoding region of 21 bp for silencing expr
         ession of the PDS gene (PDS21)-upper strand

<400>   26
tcgacttaac ttgtaaggaa tattaaggag gtaatattcc ttacaagtta ag   52

<210>   27

<211>   52

<212>   DNA

<213>   Artificial Sequence

<220>

<223>   sequence of the dsRNA encoding region of 21 bp for silencing expr
         ession of the PDS gene (PDS21)-lower strand

<400>   27
tcgacttaac ttgtaaggaa tattacctcc ttaatattcc ttacaagtta ag   52

<210>   28

<211>   115

<212>   DNA

<213>   Artificial sequence

<220>

<223>   small hairpin RNA coding region (GUS_A)

<220>

<221> misc_feature

<222> (1)..(11)

<223> SalI/PvuI restriction sites

<220>

<221> misc_feature

<222> (12)..(53)

<223> sense RNA encoding region

<220>

<221> misc_feature

<222> (54)..(62)

<223> loop structure

<220>

<221> misc_feature

<222> (63)..(104)

<223> antisense RNA encoding region

<220>

<221> misc_feature

<222> (105)..(115)

<223> SalI/PvuI restriction sites

<400> 28
gtcgacgatc gtgcggtcac tcattacggc aaagtgtggg tcaataatca ggagttcctt   60
cttcctgatt attgacccac actttgccgt aatgagtgac cgcagtcgac gatcg   115

<210> 29

<211> 112

<212> DNA

<213> Artificial sequence

<220>

<223> small hairpin RNA coding region (GUS_B)

<220>

<221> misc_feature

<222> (1)..(8)

<223> SalI/PvuI restriction sites

<220>

<221> misc_feature

<222> (9)..(50)

<223> sense RNA encoding sequence

<220>

<221> misc_feature

<222> (51)..(59)

<223> loop structure

<220>

<221> misc_feature

<222> (60)..(101)

<223> antisense RNA coding region

<220>

<221> misc_feature

<222> (102)..(112)

<223> SalI/pvuI restriction site

<400> 29

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gtcgacgatc gtcatgaaga tgcggacttg cgtggcaaag gattcgataa gttccttctt      60
tatcgaatcc tttgccacgc aagtccgcat cttcatgacg agtcgacgat cg              112
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<210> 30

<211> 115

<212> DNA

<213> Artificial sequence

<220>

<223> small hairpin RNA coding region (GUS_C)

<220>

<221> misc_feature

<222> (1)..(11)

<223> SalI/PvuI restriction sites

<220>

<221> misc_feature

<222> (12)..(53)

<223> sense RNA coding region

<220>

<221> misc_feature

<222> (54)..(62)

<223> loop structure

<220>

<221> misc_feature

<222> (63)..(104)

<223> antisense RNA encoding region

<220>

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<221>   misc_feature

<222>   (105)..(115)

<223>  .SalI/PvuI restriction sites


<400>  30
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